



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/803,344A

Source:

FEWO

Date Processed by STIC:

6/15/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202



IFWO

## RAW SEQUENCE LISTING

DATE: 06/15/2004

PATENT APPLICATION: US/10/803,344A

TIME: 17:12:18

Input Set : A:\SYR-HDAC-5005-U replacement 01.ST25.txt

Output Set: N:\CRF4\06152004\J803344A.raw

Does Not Comply  
Corrected Diskette Needed

(pg. 1-5)

There are 513 total residues, pls explain them ALL.

Invalid Response

3 <110> APPLICANT: Syrrx, Inc.  
 5 <120> TITLE OF INVENTION: HISTONE DEACETYLASE INHIBITORS  
 7 <130> FILE REFERENCE: SYR-HDAC-5005-U  
 9 <140> CURRENT APPLICATION NUMBER: US 10/803,344A  
 10 <141> CURRENT FILING DATE: 2004-03-17  
 12 <150> PRIOR APPLICATION NUMBER: US 60/455,437  
 13 <151> PRIOR FILING DATE: 2003-03-17  
 15 <150> PRIOR APPLICATION NUMBER: US 60/531,203  
 16 <151> PRIOR FILING DATE: 2003-12-19  
 18 <160> NUMBER OF SEQ ID NOS: 8  
 20 <170> SOFTWARE: PatentIn version 3.2  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 513  
 24 <212> TYPE: PRT  
 25 <213> ORGANISM: Artificial  
 27 <220> FEATURE:  
 28 <223> OTHER INFORMATION: Residues 1-482 of HDAC1 and a 6-histidine tag at the N-terminus  
 30 <400> SEQUENCE: 1  
 32 Met Ser Tyr Tyr His His His His His Asp Tyr Asp Ile Pro Thr  
 33 1 5 10 15  
 36 Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met  
 37 20 25 30  
 40 Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp Gly  
 41 35 40 45  
 44 Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His  
 45 50 55 60  
 48 Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr Arg  
 49 65 70 75 80  
 52 Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr  
 53 85 90 95  
 56 Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro  
 57 100 105 110  
 60 Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly  
 61 115 120 125  
 64 Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser  
 65 130 135 140  
 68 Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr  
 69 145 150 155 160  
 72 Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser  
 73 165 170 175  
 76 Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu  
 77 180 185 190  
 80 Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile

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81      195      200      205
84 His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
85      210      215      220
88 Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
89 225      230      235      240
92 Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
93      245      250      255
96 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
97      260      265      270
100 Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
101      275      280      285
104 Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
105      290      295      300
108 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
109 305      310      315      320
112 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile
113      325      330      335
116 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
117      340      345      350
120 Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
121      355      360      365
124 Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
125      370      375      380
128 Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
129 385      390      395      400
132 Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
133      405      410      415
136 Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Pro
137      420      425      430
140 Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
141      435      440      445
144 Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn
145      450      455      460
148 Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
149 465      470      475      480
152 Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
153      485      490      495
156 Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
157      500      505      510
160 Ala
164 <210> SEQ ID NO: 2
165 <211> LENGTH: 1542
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial
169 <220> FEATURE:
170 <223> OTHER INFORMATION: DNA sequence encoding residues 1-482 of HDAC1 and a 6-
histidine
171 tag at the N-terminus
173 <400> SEQUENCE: 2
174 atgtcgtact accatcacca tcaccatcac gattacgata tcccaacgac cgaaaacctg 60

```

There are a total of 1542 residues, please explain them all.

INVALID Response

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Input Set : A:\SYR-HDAC-5005-U replacement 01.ST25.txt

Output Set: N:\CRF4\06152004\J803344A.raw

```

176 tatttttcagg gcgccatgga acccggggga tccatggcgc agacgcaggg caccgcggagg 120
178 aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccaccca 180
180 atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga 240
182 aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc 300
184 gatgactaca ttaaattctt gcgctccatc cgtccagata acatgtcgga gtacagcaag 360
186 cagatgcaga gattcaacgt tggtagggac tgtccagtat tccatggcct gtttgagttc 420
188 tgtcagttgt ctactggtgg ttctgtggca agtgctgtga aacttaataa gcagcagacg 480
190 gacatcgctg tgaattgggc tgggggcctg caccatgcaa agaagtccga ggcactctggc 540
192 ttctgtttacg tcaatgatat cgtcttggcc atcctggaac tgctaaagta tcaccagagg 600
194 gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggagagggc cttctacacc 660
196 acggaccggg tcatgactgt gtccctttcat aagtatggag agtacttccc aggaactggg 720
198 gacctacggg atatcggggc tggcaaaggc aagtattatg ctgttaacta cccgctccga 780
200 gacgggattg atgacgagtc ctatgaggcc attttcaagc cggtcattgc caaagtaatg 840
202 gagatgttcc agcctagtgc ggtggtctta cagtgtggct cagactccct atctggggat 900
204 cggtttaggtt gcttcaatct aactatcaaa ggacacggca agtggtgtgga atttgtcaag 960
206 agctttaacc tgcctatgct gatgctggga ggcggtggtt acaccattcg taacgttgcc 1020
208 cgggtgctgga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca 1080
210 tacaatgact actttgaata ctttggacca gatttcaagc tccacatcag tcttccaat 1140
212 atgactaacc agaacacgaa tgagtacctg gagaagatca aacagcgact gtttgagaac 1200
214 cttagaatgc tgccgcacgc acctggggctc caaatgcagg cgattcctga ggacgccatc 1260
216 cctgaggaga gtggcgatga ggacgaagac gacctgaca agcgcacttc gatctgctcc 1320
218 tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg 1380
220 ggccgcaaga actcttccaa cttcaaaaaa gccaaagagag tcaaaacaga ggatgaaaaa 1440
222 gagaaagacc cagaggagaa gaaagaagtc accgaagagg agaaaaccaa ggaggagaag 1500
224 ccagaagcca aaggggtcaa ggaggaggtc aagttggcct ga 1542

```

227 &lt;210&gt; SEQ ID NO: 3

228 &lt;211&gt; LENGTH: 498

229 &lt;212&gt; TYPE: PRT

230 &lt;213&gt; ORGANISM: Artificial

232 &lt;220&gt; FEATURE:

233 <223> OTHER INFORMATION: Residues 1-488 of HDAC2 and a 6-histidine tag at the C-terminus

235 &lt;400&gt; SEQUENCE: 3

```

237 Met Gly Ser Met Ala Tyr Ser Gln Gly Gly Gly Lys Lys Lys Val Cys
238 1 5 10 15
241 Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
242 20 25 30
245 Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn
246 35 40 45
249 Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
250 50 55 60
253 Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
254 65 70 75 80
257 Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
258 85 90 95
261 Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
262 100 105 110
265 Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
266 115 120 125
269 Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His

```

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Output Set: N:\CRF4\06152004\J803344A.raw

```

270      130      135      140
273 His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
274 145      150      155      160
277 Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
278      165      170      175
281 Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
282      180      185      190
285 Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
286      195      200      205
289 Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
290      210      215      220
293 Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
294 225      230      235      240
297 Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
298      245      250      255
301 Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
302      260      265      270
305 Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
306      275      280      285
309 Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
310      290      295      300
313 Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
314 305      310      315      320
317 Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
318      325      330      335
321 Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
322      340      345      350
325 Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
326      355      360      365
329 Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
330      370      375      380
333 Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
334 385      390      395      400
337 Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
338      405      410      415
341 Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
342      420      425      430
345 Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
346      435      440      445
349 Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
350      450      455      460
353 Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr
354 465      470      475      480
357 Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
358      485      490      495
361 His His
365 <210> SEQ ID NO: 4
366 <211> LENGTH: 1497
367 <212> TYPE: DNA

```

*see pg. 5*

## RAW SEQUENCE LISTING

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Input Set : A:\SYR-HDAC-5005-U replacement 01.ST25.txt

Output Set: N:\CRF4\06152004\J803344A.raw

368 &lt;213&gt; ORGANISM: Artificial

370 &lt;220&gt; FEATURE:

371 &lt;223&gt; OTHER INFORMATION: DNA sequence encoding residues 1-488 of HDAC2 and a 6-

histidine

372 tag at the C-terminus

374 &lt;400&gt; SEQUENCE: 4

375 atgggatcca tggcgtagac tcaaggagggc ggcaaaaaaa aagtctgcta ctactacgac 60  
 377 ggtgatattg gaaattatta ttatggacag ggtcatccca tgaagcctca tagaatccgc 120  
 379 atgaccata acttgcgtgt aaattatggc ttatacagaa aaatggaaat atatagggccc 180  
 381 cataaagcca ctgccgaaga aatgacaaaa tatcacagtg atgagtatat caaatctcta 240  
 383 cggtaataa gaccagataa catgtctgag tatagtaagc agatgcagag atttaattgtt 300  
 385 ggagaagatt gtccagtgtt tgatggactc tttgagtttt gtcagctctc aactggcgggt 360  
 387 tcagttgctg gagctgtgaa gttaaaccga caacagactg atatggctgt taattgggct 420  
 389 ggaggattac atcatgctaa gaaatcagaa gcacagagat tctgttacgt taatgatatt 480  
 391 gtgcttgcca tcttgaatt actaaagtat catcagagag tcttatatat tgatatagat 540  
 393 attcatcatg gtgatgggtg tgaagaagct tttatacaaa cagatcgtgt aatgacggta 600  
 395 tcattccata aatatgggga atactttcct ggcacaggag acttgaggga tattggtgct 660  
 397 ggaaaaggca aatactatgc tgtcaatttt ccaatgagag atggtataga tgatgagtca 720  
 399 tatgggcaga tatttaagcc tattatctca aaggtgatgg agatgtatca acctagtgt 780  
 401 gtggtattac agtgtggtgc agactcatta tctggtgata gactgggttg tttcaatcta 840  
 403 acagtcaaag gtcagtctaa atgtgtagaa gttgtaaaaa cttttaactt accattactg 900  
 405 atgcttgagg gaggtggcta cacaatccgt aatggtgctc gatgttggac atatgagact 960  
 407 gcagttgccc ttgattgtga gattcccaat gagttgccat ataagatta ctttgagtat 1020  
 409 tttggaccag acttcaaact gcataattag ccttcaaaca tgacaaacca gaacactcca 1080  
 411 gaatatatgg aaaagataaa acagcggtttg tttgaaaatt tgccatggtt acctcatgca 1140  
 413 cctggtgtcc agatgcaagc tattccagaa gatgctgttc atgaagacag tggagatgaa 1200  
 415 gatggagaag atccagacaa gagaatttct attcgagcat cagacaagcg gatagcttgt 1260  
 417 gatgaagaat tctcagattc tgaggatgaa ggagaaggag gtcgaagaaa tgtggctgat 1320  
 419 cataagaaag gagcaagaa agctagaatt gaagaagata agaaagaaac agaggacaaa 1380  
 421 aaaacagacg ttaaggaaga agataaatcc aaggacaaca gtggtgaaaa aacagatacc 1440  
 423 aaaggaacca aatcagaaca gctcagcaac cccgggcata accatcacca tcaactaa 1497

426 &lt;210&gt; SEQ ID NO: 5

427 &lt;211&gt; LENGTH: 782

428 &lt;212&gt; TYPE: PRT

429 &lt;213&gt; ORGANISM: Artificial

431 &lt;220&gt; FEATURE:

432 <223> OTHER INFORMATION: Residues 73-845 of HDAC6 and a 6-histidine tag at the C-

terminus

434 &lt;400&gt; SEQUENCE: 5

436 Met Pro Gly Met Asp Leu Asn Leu Glu Ala Glu Ala Leu Ala Gly Thr  
 437 1 5 10 15  
 440 Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp  
 441 20 25 30  
 444 Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln  
 445 35 40 45  
 448 Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg  
 449 50 55 60  
 452 Phe Ala Glu Lys Glu Glu Leu Met Leu Val His Ser Leu Glu Tyr Ile  
 453 65 70 75 80  
 456 Asp Leu Met Glu Thr Thr Gln Tyr Met Asn Glu Gly Glu Leu Arg Val  
 457 85 90 95

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 06/15/2004  
PATENT APPLICATION:    US/10/803,344A      TIME: 17:12:19

Input Set : A:\SYR-HDAC-5005-U replacement 01.ST25.txt  
Output Set: N:\CRF4\06152004\J803344A.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8

**VERIFICATION SUMMARY**

DATE: 06/15/2004

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Input Set : A:\SYR-HDAC-5005-U replacement 01.ST25.txt

Output Set: N:\CRF4\06152004\J803344A.raw